

<110> BROWN, Eric L. LEE, Lawrence HOOK, Magnus

<120> METHOD OF PREVENTING T CELL-MEDIATED RESPONSES BY THE USE OF THE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II ANALOG PROTEIN (MAP PROTEIN) FROM STAPHYLOCOCCUS AUREUS

EQUENCE LISTING

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aca at Thr Il															96	
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aaa to Lys Se 50	r Val														192	
ctt to Leu Se 65															240	
aga gt Arg Va															288	

d , ,	,					•											
,	aca Thr	agt Ser	gac Asp	att Ile 100	aaa Lys	gca Ala	att Ile	agt Ser	gtt Val 105	aac Asn	gta Val	gat Asp	act Thr	aaa Lys 110	aag Lys	caa Gln	336
	gtg Val	aaa Lys	gat Asp 115	aaa Lys	gag Glu	gca Ala	aaa Lys	gca Ala 120	aat Asn	gtt Val	caa Gln	gtg Val	ccg Pro 125	tat Tyr	aca Thr	atc Ile	384
		gtg Val 130															432
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		tta Leu															528
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	Phe	Asn	Lys 35	Asn	Gln	Gln	Ile	Ser 40	Tyr	Lys	Asp	Ile	Glu 45	Asn	Lys	Val	
	Lys	Ser 50	Val	Leu	Tyr	Phe	Asn 55	Arg	Gly	Ile	Ser	Asp 60	Ile	Asp	Leu	Arg	
	Leu 65	Ser	Lys	Gln	Ala	Lys 70	Tyr	Thr	Val	His	Phe 75	Lys	Asn	Gly	Thr	Lys 80	

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	Arg Val Val Asp Leu Lys Ala 85	a Gly Ile His Thr Ala Asp Leu Ile Asn 90 95
	Thr Ser Asp Ile Lys Ala Ile 100	e Ser Val Asn Val Asp Thr Lys Lys Gln 105 110
	Val Lys Asp Lys Glu Ala Lys 115	s Ala Asn Val Gln Val Pro Tyr Thr Ile 120 125
	Thr Val Asn Gly Thr Ser Glr 130 135	n Asn Ile Leu Ser Asn Leu Thr Phe Lys 5 140
	Lys Asn Gln Gln Ile Ser Tyr 145 150	r Lys Asp Leu Glu Asn Asn Val Lys Ser 155 160
	Val Leu Lys Ser Asn Arg Gly 165	y Ile Thr Asp Val Asp Leu Arg Leu Ser 170 175
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	Ile Asp Leu Lys Ala Gly Ile 195	e Tyr 200
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		a agc caa aac att tta tca agc tta aca r Ser Gln Asn Ile Leu Ser Ser Leu Thr 25 30
		t agt tat aaa gat ata gag aat aaa gtt e Ser Tyr Lys Asp Ile Glu Asn Lys Val 40 45
	aaa tca gtt tta tac ttt aat	t aga ggt att agt gat atc gat tta aga

Lys	Ser 50	Val	Leu	Tyr	Phe	Asn 55	Arg	Gly	Ile	Ser	Asp 60	Ile	Asp	Leu	Arg		
ctt Leu 65	tct Ser	aag Lys	caa Gln	gca Ala	aaa Lys 70	tac Tyr	acg Thr	gtt Val	cat His	ttt Phe 75	aag Lys	aat Asn	gga Gly	aca Thr	aaa Lys 80	;	240
aga Arg	gtt Val	gtc Val	gat Asp	ttg Leu 85	aaa Lys	gca Ala	ggc Gly	att Ile	cac His 90	aca Thr	gcc Ala	gac Asp	tta Leu	atc Ile 95	aat Asn		288
	agt Ser																336
gtg Val	aaa Lys	gat Asp 115	aaa Lys	gag Glu	gca Ala	aaa Lys	gca Ala 120	aat Asn	gtt Val	gtc Val	gac Asp	ctg Leu 125	cag Gln	cca Pro	agc Ser	-	384
	att Ile 130	_	tga														396
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Met 1		Gly		5					10					15			
Met 1 Thr	Arg	Gly	Val 20	5 Asn	Gly	Thr	Ser	Gln 25	10 Asn	Ile	Leu	Ser	Ser 30	15 Leu	Thr		
Met 1 Thr	Arg	Gly Thr Lys 35	Val 20 Asn	5 Asn Gln	Gly	Thr	Ser Ser 40	Gln 25 Tyr	10 Asn Lys	Ile Asp	Leu Ile	Ser Glu 45	Ser 30 Asn	15 Leu Lys	Thr Val		
Met 1 Thr Phe	Arg Ile Asn	Gly Thr Lys 35	Val 20 Asn Leu	5 Asn Gln Tyr	Gly Gln Phe	Thr Ile Asn 55	Ser Ser 40	Gln 25 Tyr Gly	10 Asn Lys Ile	Ile Asp Ser	Leu Ile Asp	Ser Glu 45	Ser 30 Asn Asp	Leu Lys	Thr Val		
Met 1 Thr Phe Lys Leu 65	Arg Ile Asn Ser 50	Gly Thr Lys 35 Val	Val 20 Asn Leu Gln	5 Asn Gln Tyr Ala	Gly Gln Phe Lys 70	Thr Ile Asn 55	Ser Ser 40 Arg	Gln 25 Tyr Gly Val	10 Asn Lys Ile	Ile Asp Ser Phe	Leu Ile Asp 60 Lys	Ser Glu 45 Ile	Ser 30 Asn Asp	Leu Lys Leu Thr	Thr Val Arg		

Val Lys Asp Lys Glu Ala Lys Ala Asn Val Val Asp Leu Gln Pro Ser 115 120 125

Leu Ile Ser 130